Atty Dkt. No.: 10050845-1
USSN: 10/815,102

AMENDMENT

Please incorporate the following amendments into the subject application.

In the Claims:

1. (Currently Amended) A method of using statistical analysis of genetic data **from an inbred population** to determine likely genetic regions for a recessive genetic disease or trait, comprising the steps of:

obtaining actual genotype data ~~for one or more affected~~ **from members of an inbred population, wherein said members are selected from one or both of:** people ~~with the~~ **affected with a** genetic disease or trait in ~~a~~ **said inbred** population~~, for their parents, or for the affected people and their parents~~**and parents of people affected with said genetic disease or trait in said inbred population**;

obtaining estimated genotype data for ~~the~~ **said inbred** population; and

analyzing the actual and estimated genotype data to find a region in genomes of the affected people that includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly, wherein ~~the~~ **said** step of analyzing is performed using a computing device, and **wherein said step of analyzing** ~~further~~ comprises:

determining a set of scores under various assumptions for each **of said markers** ~~marker~~ in ~~the~~ **said actual and estimated** genotype data relative to each person for which actual genotype data was determined, with the assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous;

merging the set of scores for each marker to arrive at a first merged score for each marker, the first merged score being determined under an assumption that the marker is autozygous, and a second merged score for each marker, the second merged score being determined under an assumption that the marker is not autozygous;

~~first assigning to each said marker a first computed action of said first merged score and said second merged score~~ **computing for each of said markers a ratio of said first merged score to said second merged score to produce marker**

scores, wherein each of said ~~first computed function~~ marker scores indicates ~~indicating~~ at least in part a statistical distinction between whether said marker is autozygous and whether said marker is not autozygous;

~~second assigning to each one of a plurality of sequential regions of markers a second computed function of those markers in each one particular sequential region, said second computed function being responsive to said steps of first assigning; and~~

~~identifying at least one particular said region of markers in response to a result of said steps of second assigning, said at least one particular region of markers having an assigned result of said computed function that is substantially at least the next-to-highest result of said computed function~~

examining said marker scores to determine one or more contiguous regions of markers with a high sum of marker scores;

selecting from said one or more contiguous regions of markers at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and

reporting said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a user of said computing device.

2. (Currently Amended) A method as in claim 1, wherein ~~the~~ said inbred population is a relatively inbred population with a higher occurrence of ~~the~~ said genetic disease or trait than a more general population.

3. (Currently Amended) A method as in claim 2, wherein the particular homozygous pairs of alleles are autozygous alleles descended from a founder of ~~the~~ said genetic disease or trait in ~~the~~ said relatively inbred population.

4. (Currently Amended) A method as in claim 3, wherein ~~a~~ said marker score for a marker represents a comparison of a likelihood of observing ~~the~~ said marker given

that people with ~~the~~ **said** genetic disease or trait are autozygous at ~~the~~ **said** marker versus a likelihood of observing ~~the~~ **said** marker given that alleles for ~~the~~ **said** marker are independent of ~~the~~ **said** genetic disease or trait.

5. (Currently Amended) A method as in claim 4, wherein ~~the~~ **said** marker receives a higher **marker** score from one form of homozygosity versus another form of homozygosity, with the form receiving ~~the~~ **said** higher score being more likely to be associated with ~~the~~ **said** genetic disease or trait.

6. (Currently Amended) A method as in claim 5, wherein ~~the~~ **said** ~~merged~~ **marker** scores are placed in an array ordered by a chromosomal order of markers associated with the scores.

7. (Currently Amended) A method as in claim 6, wherein identifying said at least one particular region further comprises determining a consecutive portion of ~~the~~ **said** array that has the highest sum.

8. (Currently Amended) A method as in claim 6, wherein identifying said at least one particular region further comprises computing all sums of a predetermined fixed number of adjacent elements in ~~the~~ **said** array and comparing the sums.

9. (Cancelled)

10. (Currently Amended) A method as in claim ~~9~~ **6**, further comprising the step of locating a statistically significant gap in ~~the scores~~ **said sums** for non-overlapping regions, wherein regions having ~~scores~~ **sums** above the gap are ~~determined to be the one or more additional regions of markers~~ **selected and reported to said user**.

11. (Currently Amended) A method of analyzing actual and estimated genotype data, with the actual genotype data obtained for one or more affected people with the

genetic disease or trait in ~~a~~ an inbred population, for their parents, or for the affected people and their parents, and with the estimated genotype data obtained for ~~the~~ said population, the method performed to find a region in genomes of the affected people that includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly, the method comprising:

determining a set of scores under various assumptions for each marker in ~~the~~ said actual and estimated genotype data relative to each person for which actual genotype data was determined, with the assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous;

merging the set of scores for each marker to arrive at a first merged score for each marker, the first merged score being determined under an assumption that the marker is autozygous, and a second merged score for each marker, the second merged score being determined under an assumption that the marker is not autozygous;

~~first assigning to each said marker a first computed action of said first merged score and said second merged score~~ computing for each of said markers a ratio of said first merged score to said second merged score to produce marker scores, wherein each of said ~~first computed function~~ marker scores indicates ~~indicating~~ at least in part a statistical distinction between whether said marker is autozygous and whether said marker is not autozygous;

~~assigning to each one of a plurality of sequential regions of markers a second computed function of those markers in each one particular sequential region, said second computed function being responsive to said steps of first assigning; and~~

~~identifying at least one particular said region of markers in response to a result of said steps of second assigning, said at least one particular region of markers having an assigned result of said computed function that is substantially at least the next-to-highest result of said computed function;~~

examining said marker scores to determine one or more contiguous regions of markers with a high sum of marker scores;

selecting from said one or more contiguous regions of markers at least one

contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and

reporting said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a user of said computing device;

wherein ~~the~~ **said** determining ~~steps~~ and ~~the~~ merging ~~step~~ **steps** are performed using a computing device.

12. (Currently Amended) A method as in claim 11, wherein ~~the~~ **said** population is a relatively inbred population with a higher occurrence of ~~the~~ **said** genetic disease or trait than a more general population.

13. (Currently Amended) A method as in claim 12, wherein the particular homozygous pairs of alleles are autozygous alleles descended from a founder of ~~the~~ **said** genetic disease or trait in ~~the~~ **said** relatively inbred population.

14. (Currently Amended) A method as in claim 13, wherein ~~a~~ **said marker** score for a marker represents a comparison of a likelihood of observing ~~the~~ **said** marker given that people with ~~the~~ **said** genetic disease or trait are autozygous at ~~the~~ **said** marker versus a likelihood of observing ~~the~~ **said** marker given that alleles for the marker are independent of ~~the~~ **said** genetic disease or trait.

15. (Currently Amended) A method as in claim 14, wherein ~~the~~ **said** marker receives a higher **marker** score from one form of homozygosity versus another form of homozygosity, with the form receiving ~~the~~ **said** higher score being more likely to be associated with ~~the~~ **said** genetic disease or trait.

16. (Currently Amended) A method as in claim 15, wherein ~~the~~ **said** ~~merged~~ **marker** scores are placed in an array ordered by a chromosomal order of markers associated with the scores.

17. (Currently Amended) A method as in claim 16, wherein identifying said at least one particular region further comprises determining a consecutive portion of ~~the~~ **said** array that has the highest sum.

18. (Currently Amended) A method as in claim 16, wherein identifying said at least one particular region further comprises computing all sums of a predetermined fixed number of adjacent elements in ~~the~~ **said** array and comparing the sums.

19. (Cancelled)

20. (Currently Amended) A method as in claim ~~19~~ **16**, further comprising the step of locating a statistically significant gap in ~~the scores~~ **said sums** for non-overlapping regions, wherein regions having ~~scores~~ **sums** above the gap are ~~determined to be the one or more additional regions of markers~~ **selected and reported to said user**.

21. (Currently Amended) An apparatus including:

a processor;

input and output interfaces; and

a memory storing instructions executable by the processor to analyze actual and estimated genotype data, with the actual genotype data obtained for one or more affected people with the genetic disease or trait in ~~a~~ **an inbred** population, for their parents, or for the affected people and their parents, and with the estimated genotype data obtained for ~~the~~ **said** population, the method performed to find a region in genomes of the affected people that includes markers exhibiting particular homozygous pairs of alleles more frequently than would occur randomly, the instructions including steps of: (a) determining a set of scores under various assumptions for each marker in ~~the~~ **said actual and estimated** genotype data relative to each person for which actual genotype data was determined, with the assumptions for each marker including at least that the marker is autozygous and that the marker is not autozygous; (b) merging the

set of scores for each marker to arrive at a **first** merged score for each marker, ~~with~~ the **first merged score being determined** ~~scores that are merged for each marker including at least scores~~ under an assumption that the marker is autozygous**, and a second merged score for each marker, the second merged score being determined** ~~and scores~~ under an assumption that the marker is not autozygous; (c) ~~determining a region of markers that has a highest or next-highest run of merged scores; and (d) sequencing the region of markers that has said highest or next-highest run of merged scores~~ **computing for each of said markers a ratio of said first merged score to said second merged score to produce marker scores, wherein each of said marker scores indicates at least in part a statistical distinction between whether said marker is autozygous and whether said marker is not autozygous; (d) examining said marker scores to determine one or more contiguous regions of markers with a high sum of marker scores; (e) selecting from said one or more contiguous regions of markers at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait; and (f) reporting said at least one contiguous region likely to contain a recessive allele associated with said genetic disease or trait to a user of said computing device**.

22. (Currently Amended) A method as in claim 1, further comprising the step of sequencing said at least one ~~particular region of markers~~ **contiguous region likely to contain a recessive allele associated with said genetic disease or trait**.

23. (Currently Amended) A method as in claim 11, further comprising the step of sequencing said at least one ~~particular region of markers~~ **contiguous region likely to contain a recessive allele associated with said genetic disease or trait**.